



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/954773  
Source: OIPF  
Date Processed by STIC: 10/09/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

# Raw Sequence Listing Error Summary

| ERROR DETECTED  | SUGGESTED CORRECTION   | SERIAL NUMBER: 09/954773 |
|---|--|--------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO |  |                          |
| 1 _____ Wrapped Nucleics<br>Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."   |                          |
| 2 _____ Invalid Line Length   | The rules require that a line not exceed 72 characters in length. This includes white spaces.  |                          |
| 3 _____ Misaligned Amino<br>Numbering   | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  |                          |
| 4 _____ Non-ASCII   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.   |                          |
| 5 _____ Variable Length   | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.   |                          |
| 6 _____ PatentIn 2.0<br>"bug"   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.   |                          |
| 7 _____ Skipped Sequences<br>(OLD RULES)  | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |                          |
| 8 _____ Skipped Sequences<br>(NEW RULES)  | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br><210> sequence id number<br><400> sequence id number<br>000   |                          |
| 9 <input checked="" type="checkbox"/> Use of n's or Xaa's<br>(NEW RULES)                    | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |                          |
| 10 _____ Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence   |                          |
| 11 _____ Use of <220>   | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)   |                          |
| 12 _____ PatentIn 2.0<br>"bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |                          |
| 13 _____ Misuse of n  | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.  |                          |

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001

TIME: 08:45:40

Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

3 <110> APPLICANT: Lighfoot, David A.  
 4 Gibson, Paul T.  
 5 Merkem, Khalid  
 7 <120> TITLE OF INVENTION: Soybean Sudden Death Syndrome Resistant Soybeans,  
 8 Soybean Cyst Nematode Resistant Soybeans and Methods of  
 9 Breeding and Identifying Resistant Plants  
 11 <130> FILE REFERENCE: Sou Illinois 1268/2 Sequence Listing  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/954,773  
 C--> 14 <141> CURRENT FILING DATE: 2001-09-18  
 16 <150> PRIOR APPLICATION NUMBER: 60/035,335  
 17 <151> PRIOR FILING DATE: 1997-01-14  
 19 <160> NUMBER OF SEQ ID NOS: 20  
 21 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

689 <210> SEQ ID NO: 9  
 690 <211> LENGTH: 801  
 691 <212> TYPE: DNA  
 692 <213> ORGANISM: Glycine max  
 694 <400> SEQUENCE: 9  
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 696 ttcgtcgacc tcgagggatc acgctaataga tatattatta atcaactgct tcaatagagt 120  
 697 gcacacaccc tatctttcat aaaattacta cactttttta tttttgtaat aaaaaaccta 180  
 698 gaaaaactca ttatgaaaca gatgatgtac ttttaacact ctgtcggcct ctctctctct 240  
 699 attatatatt gatttaaatt tattgagaat tatatttttg ttgggtctca tttattatat 300  
 700 tttattaatt ggatccgggc cctctagatg cggccgcgat cataagcttg agtattctat 360  
 701 agtgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttcctatg tgaaattgtt 420  
 E--> 702 atccgctcac aattccacac aacatacagc ccggaagcat aaagtgt<sup>3</sup>naa gcctgggg<sup>3</sup>tn 480  
 E--> 703 cctaatagagt gagctaactc acattaattg ccttgcgctc actgcccgtt ttccagtcng 540  
 E--> 704 gaaacctgtc ctgccagctg cattaatgaa tcngccaacc cncggggana agcngtttgc 600  
 E--> 705 ntatgggcgc tcttncgcgt tctcgcgtca ntgactcgct gcgctcngtc nttcngntgc 660  
 E--> 706 cgcgaacggt atcancncac tcnaangnng taaatacggg tatccaccna accnngggga 720  
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 711 <211> LENGTH: 809  
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 713 <213> ORGANISM: Glycine max  
 715 <400> SEQUENCE: 10  
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 717 ccgagctcga attcgtcgac ctcgagggat ctttttatgt tggtagctac tgtaatatca 120  
 718 tcttgtaactt ttaactttta agtcatactc cttttggact catatataag caaaagagt 180  
 719 gtcttgatag tcggacttaa atataagcaa atctaactaa tttgtccta ttttaacttt 240  
 720 tcattcctaa aacacccttc atttaattct aattctattt ccaataactc ttttttat<sup>3</sup>tc 300  
 721 atgataacaa gttccaatga aggacatttt agaaataacc ttatttttta tttgagatta 360

*Errored  
Must enumerate n's*

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Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

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E--> 724 ctttttaatt catctttgct gcatanctac ttagctactg tgctctgac cgggccctct 540
725 agatgcggcc gcatgcataa gcttgagtat ctatagtgtc cctaaatagc ttggcgatc 600
E--> 726 atggtcatag ctgtttccng tgtgaaattg ttatccgctc acaattccac acaacatacg 660
E--> 727 anccggaagc ataaaagtgt taagccnggg gtgcctaag agtgagctaa ctcacattaa 720
E--> 728 ttgcgttgcg ctactgccc gcttccnatt cgggaaactg tcctgncanc tgcattaatg 780
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732 <211> LENGTH: 810
733 <212> TYPE: DNA
734 <213> ORGANISM: Glycine max
736 <400> SEQUENCE: 11
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738 aattcgtcga cctcgagggg tctataatat ttctgacagc taccttttta tttagcttgc 120
739 agaggggctg attttgagga aaacatcatc catggtataa agtcggttta gattccagct 180
740 attgttcaca ttcattccctt acatatgaga atatccctat aagctgaaac taacttttac 240
741 aaacaaacat gcaccgaacc attaaagttt gacttaatat cgggggtata atgaccttaa 300
742 ttcagaaatt cacataaata actaaaagta agttgtattt ttttatgtc tggatttact 360
743 gcacaaacta aacaaaagtt tgtggattta gacataaaaa ataccaatgc tgtgtgaaaa 420
E--> 744 taagaaatgg tggtcataata gacaagtttc tttctgttt tctttaaatt gcagtcnaag 480
E--> 745 ccatcangag gttcatgtaa ttaaccaaac tagacgttga cttttggttt tatccttttg 540
746 tagaatagca agcaagtcac tataaatctg gccattggga cagcttagtt taactcccgc 600
E--> 747 cgcaaatattg ttaaaatatt naataataat atcacctaaa atcatatttg tcanttcatt 660
E--> 748 ttgttttang ttatatcaat tattattttt taccttacnt cctttataat ntcaatgatg 720
E--> 749 ggacccaaaa aattatcaaa tacnttnaag cnttatttat tattaattaa ncctttaatt 780
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753 <211> LENGTH: 777
754 <212> TYPE: DNA
755 <213> ORGANISM: Glycine max
757 <400> SEQUENCE: 12
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759 catctagagg gcccgatct ttcggttgaa gcaaaattga agtcttttgc tcatttttat 120
760 caaattcttt aatgaaaagt taattacata aaatatatta gtagaagcaa ttttacacag 180
761 ttattattta aaaaaattac acagttattc aataacaaat tacaatata tataaggtta 240
762 taataaatat tttaaaattc atataaaaga tgacttatta ataagttgat aatgtaaatt 300
763 ttttacacta ttaactcat tttacgtaat cttagcgaca acatactatt tttttcatga 360
764 aatttacaaa aagctttcaa aaataaaatt attagttgta cccccaaaat ataaaattat 420
765 tagctatgtt aaaaatttgt gaatttcata aaagaaaaaa atattacagt attatatatt 480
766 aaaattaaat ctacacaataa aaacacgtaa agttatcggt ttgaattatt agttaagtc 540
E--> 767 cttcgtctcg tatttttctc aactctaccg acagcataaa caggttgctc cttcntaat 600
E--> 768 aacaatcgtg gctgggaaca aaaatcgttt ttttagaaga atcngaaatc gtattgacgg 660
E--> 769 tgcgttttaa aaagactatc caataatctt cttttaataa cnctgaattt cnccaattct 720
E--> 770 tncncaacgg ttttttggtg cgttntttta aaaaaagttt aatttaatta aaatncn 777
772 <210> SEQ ID NO: 13
773 <211> LENGTH: 775
774 <212> TYPE: DNA
775 <213> ORGANISM: Glycine max

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001

TIME: 08:45:40

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Output Set: N:\CRF3\10092001\I954773.raw

777 &lt;400&gt; SEQUENCE: 13

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E--> 778 atncccnagc tattaggtga cactatagaa tactcaagct tatgcatgcg gccgcatcta 60
E--> 779 gagggccccg atccaattaa taaaatataa taaatgagac caacnaaaat atattctcna 120
E--> 780 taaatttnaa tccatatttt antaaaaaaa aaaaggccna caaatntta aaattcctnc 180
E--> 781 nncnntttca tantnatttt tcctaggttt tttattncaa aanttataaaa ttntattant 240
E--> 782 tttatnaaaa atagggtntn tgcacnctat tgaaccantn nattaataat atatctttan 300
E--> 783 cntnatccct caaggtcaac aaanttcana ncncggccna cttggccaat tcncctata 360
E--> 784 gtgantcntn ttacaactca ctggcgctcg ttttacaacc tcgtgactgg gaaanccctg 420
E--> 785 gcggtcccca anttaatenc cttgcaacat ntcccccttc gccngctggg gttnataccn 480
E--> 786 aaaaggcccc cnccgatcgc ccttcccnac ttttgcgccc cctnaatggc naatggacgc 540
E--> 787 ccctgttncg ngencattan ncggggcggtg tgtggtggtt acccccacnt gaccctacac 600
E--> 788 ttgccagccc cctaaccenc cccctttcgc tttctccctt ccttttctcg ccnettcgcc 660
E--> 789 ggnttccent caagcnctaa atcggggctc cctttagggt tccnaattaa ttgctttacg 720
E--> 790 gccctccacc ccaaaaactt gataagggtg atggtcnent tctggggcnn ccccn 775

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792 &lt;210&gt; SEQ ID NO: 14

793 &lt;211&gt; LENGTH: 796

794 &lt;212&gt; TYPE: DNA

795 &lt;213&gt; ORGANISM: Glycine max

797 &lt;400&gt; SEQUENCE: 14

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E--> 798 acntgattca ccaagctatn taggtgacta tagaatactc aagcttatgc atgcggccgc 60
799 atctagaggg cccggtacag agcacagtag ctaagtagct atgcagcaaa gatgaattaa 120
800 aaagaagcat ataatacatt ttagtacatt tgtgaaattt ggtactccct ttggactcgt 180
801 atataagaaa aaataactaa tttcacatta attaagaaag ttagttcaca tcatttaatt 240
802 ttactaatct caaataaaaa ataaggttat ttctaaaatg tccttcattg gaacttgta 300
803 tcatgaataa aaaagagtta ttggaaatag aattagaatt aaatgaaggg tgttttagga 360
804 atgaaagtat taaataggac aaaattagtt agatttgctt atatttaagt ccgacataca 420
E--> 805 agaccactct tttgcttata tatgagtcca aaggaggatg gacttaaaag ttnaaagtnc 480
806 aagatgatat tacagtagct accaacataa aaagatccct cgaggtcgac gaattcgagc 540
807 tcggccgact tggccaattc ccttatagtg agtcgtatta caattcactg gccgtcgttt 600
E--> 808 tacaacgtcn tgactgggaa aacctggcgt tccccactta tcgccttgca gcacatcccc 660
E--> 809 tttcgccngc tggcgtnnta ccaaaaaggc cgcaccgatc gcccttcccn acagttgcc 720
E--> 810 cncctgaat ggcgaatatg acccccctgt taccggccca tttaaaccce gnnnggtggt 780
E--> 811 gtggttnccc cncen 796

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813 &lt;210&gt; SEQ ID NO: 15

814 &lt;211&gt; LENGTH: 782

815 &lt;212&gt; TYPE: DNA

816 &lt;213&gt; ORGANISM: Glycine max

818 &lt;400&gt; SEQUENCE: 15

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819 attacgccaa gctattaggt gacactatag aaatactcaa gcttatgcat gcggccgcat 60
820 cttagagggc cggatctttt attaaaaatt taattgagtc tcttaattat tgaaaagttt 120
821 aattaaatca tcaattatta aaaaaaatca accatatcct ttattgttta aaacattata 180
822 attatgctct ttcaaccaac tctgttagtt taattgatag aagttttgta aatagatatt 240
823 tttacataat ataaataatc tttttacata tattgcagcc aatgtaaaat attatctttt 300
824 tacattcatt gcttttgatg taaaaaatta ttgttttaca tatgttgat tgacaataaa 360
825 tataaaaaata tttatttttg tcaattagat taatgaactg atgatgaaaa agatataatt 420
826 ataataatatt taataattag agaatttgat tgaacttttt aataattaa aaattaaatg 480
827 aatttttaatt tataattaa gggattaatt atatatata gctttaatgt atttataatt 540
E--> 828 tttggtgtcc ncattaatat tataaaagga tgtaagtaaa aaataataat taatattaca 600
829 taaacaaaat aaaatgacaa tattattagg tgatattatt attaatattt taaacaaatt 660

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## RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/954,773

TIME: 08:45:40

Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

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832 tt 782
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836 <212> TYPE: DNA
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842 cgccctgtag cggcgcatga agcgcggcgg gtgtgggtgg tacgcgcagc gtgaccgcta 180
843 cacttgccag cgccctagcg cccgcctcct tcgctttcct ccccttcctt ctgcgccagt 240
844 tcgcgcggct tcccgcgtca gctctaaatc gggggctccc tttagggttc cgatttagtg 300
E--> 845 ctttacggca cctcgacccc aaaaacttg attagggtga tggttcacgt antgggcat 360
E--> 846 cgccctgata gacngttttt cgcccttga cnttggagtc cacgttcttt aatagtggac 420
847 tcttgttcca aactggaaca aactcaacc ctatctcggt ctattctttt gatttataag 480
E--> 848 ggattttgcc gatttcggcc tattggttaa aaaatgagct gatttaacaa aaatttnacg 540
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E--> 850 atctgtncgg tatttccacc gcataatgtg cactctcaat acaatctgct ctgatccnca 660
E--> 851 taatttaanc canccccgaa acccgcccaa cacccttaa aacnccctta acgggcttgt 720
E--> 852 ntgctcccg cgatcgctta acaanaaac ttttaaactg ntcccggaac ngcatntttt 780
E--> 853 naaagttttc accncctcc c 801
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856 <211> LENGTH: 798
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858 <213> ORGANISM: Glycine max
860 <400> SEQUENCE: 17
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862 gcatctagag ggcccgatcg gcccttccca acagttgcgc agcctgaatg gcgaatggac 120
E--> 863 gcgcccgtga gcggcgcat aagcgcggcg ggtgtggtgg ttacgcnan cgtgaccgct 180
864 acatttgcca gcgcctagc gccgcctcct ttcgctttct tcccttcctt tctgcgccag 240
865 ttgcgcggct tcccgcgtca agctctaaat cgggggctcc ctttagggtt ccgatttagt 300
E--> 866 gctttacggc acctcnacce cnaaaaactt gattagggtg atggttcacg tattgggcca 360
E--> 867 tcnccctgat agacagtttt tcgccnttg acgttggagt ccacgttctt taatattgga 420
868 ccttgttcca aactggaaca aactcaacc ctatctcggt ctattctttt gatttataag 480
E--> 869 ggattttgcc natttcggcc natnggttaa aaaatgagct natttaacna aaatttaacg 540
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877 <211> LENGTH: 796
878 <212> TYPE: DNA
879 <213> ORGANISM: Glycine max
881 <400> SEQUENCE: 18
E--> 882 acggnttntg aatngttatt taggtgacac tatagaaata ctcaagctta tgcatgcggc 60
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TIME: 08:45:40

Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

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E--> 887 gaaatncctn acctttacca cctcnaggac aagtggctct cncggggcgac nggtattgatn 360
E--> 888 acngttaccc ggaagatacc cagattgagc cccacttac taagacnaag cccaacgtn 420
E--> 889 cccctcnaga cctgtctctt gaatgactac nanactgact cnangaagaa gctccaacca 480
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E--> 892 ccnnagggtta cnttactccc tcccnctct ctanatttcc tntangaagc tgccttcccc 660
E--> 893 cnaaattagg ggccattctc ttcctttccc gtcttttccac tccctctctgc tcttatcnng 720
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      897 <210> SEQ ID NO: 19
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      900 <213> ORGANISM: Glycine max
      902 <400> SEQUENCE: 19
E--> 903 acggcagtg ntgtaatncg actcactata gggcgaattg gccaaagtcgg ccgagctcga 60
      904 attcgtcgac ctcgagggat cgcgaagta tctactcaac tatcagaggt agttggcgctc 120
E--> 905 atcgagcgcc atctcgaacc gacgttgctg gccgtacatt tgtacngctc cgcngtggat 180
E--> 906 ggcggcctga agccacacng tgatattgat ttgctgggta cngtgaccgt aaggcttgat 240
E--> 907 gaaacnacgc ggcgagcttt gatccacnat gcccatnacc nagagtagac cagaatctaa 300
E--> 908 cacnaatcnc attgtcngat ataacnaaat gctttttaac acgagtgtt cccctnacan 360
E--> 909 tgtagattt gageccanct cccttctcaa tgatacatnc aggatgaacn ntttgacatn 420
E--> 910 nctccaccna tttggnagtc tcatgcacca ccacattccc ncagtatgtt tgaaggctnt 480
E--> 911 tggccngttc cettananaa atattcctcc gccnnttcag gttgantctc attccnnaaa 540
E--> 912 atatataccc ttgtccattt ccactcncaa ttctnctgt tngaaagaac ntttgcttcc 600
E--> 913 agcnttcttc ccaaancnat ttttnggaaa ccctctgttt tcnaagaaat tgggttcanc 660
E--> 914 tccaattctn tccattccna aggggttccct ccactttaac cccgnatnan caaccaaggg 720
E--> 915 gaattgaaaa aacgggaaag ggaaaaaaat ngggcctact tncaggga nggcgcccc 780
E--> 916 tcaagnaat ttncaaagaa gnananaa 808
      918 <210> SEQ ID NO: 20
      919 <211> LENGTH: 787
      920 <212> TYPE: DNA
      921 <213> ORGANISM: Glycine max
      923 <400> SEQUENCE: 20
E--> 924 ngncgacgcc ngtgnatgac cactataggg cgaattggcc aagtcggccg agctcgaatt 60
      925 cgtcgacctc gagggatcta tatataggct tgctaagggt agagagagga agactagaga 120
E--> 926 tttggatcna caatgccaat aacaaagagt tnaccagaat cnaacacaaa tcnattgtc 180
E--> 927 ngatataaca aaatgctttt taacacgagt gcttcacata acagtgtng atttgagccc 240
E--> 928 aactccttcc tcaatgatac atccnggatg gaccaatttg acatgcatca ccnatttggc 300
E--> 929 agtctcatgc acaaccacat tccccacant atgtntgang gtcattggcc ngttcactaa 360
E--> 930 ganaattatt cctccccagt tcangtnag tctcantcnn naaatatagt cctttgtcc 420
E--> 931 natttccntc tnaaatcctt cctgtggaaa gaccattgca tncagcttcc tatcngaaac 480
E--> 932 aatatttgga aacccctctg tcttccaaga aatnggtgtc cnetcnattc tntccatac 540
E--> 933 cnaagggttc atccagttta cctgattag ancnnagggt agtggaanaa ccgggaaagg 600
E--> 934 aanaaaatng gccnacttcc aaggaaggcc cctcctnag aaaattttga gagagagaga 660
E--> 935 agagtctctt nacctttgccc tgcctcntta tattantcca gtnttatncc cncnanggtg 720
E--> 936 gttaccnaan ctttttcnc cnaatacngt ctactaatt tggctactacc cncctctn 780
E--> 937 gtaccan 787

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001

TIME: 08:45:41

Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:695 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9  
M:340 Repeated in SeqNo=9  
L:716 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
M:340 Repeated in SeqNo=10  
L:737 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11  
M:340 Repeated in SeqNo=11  
L:758 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12  
M:340 Repeated in SeqNo=12  
L:778 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13  
M:340 Repeated in SeqNo=13  
L:798 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14  
M:340 Repeated in SeqNo=14  
L:828 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
M:340 Repeated in SeqNo=15  
L:845 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
M:340 Repeated in SeqNo=16



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001

TIME: 08:45:41

Input Set : A:\2seqlist.app

Output Set: N:\CRF3\10092001\I954773.raw

L:861 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17  
M:340 Repeated in SeqNo=17  
L:882 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18  
M:340 Repeated in SeqNo=18  
L:903 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19  
M:340 Repeated in SeqNo=19  
L:924 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
M:340 Repeated in SeqNo=20